NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CAR §1.821 - §1.825 for the following reasons(s):

[ ]   1.   This application clearly fails to comply with the requirements of 37 CAR §1.821 - §1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990, and at 55 FR 18230, May 1, 1990.

[ ]   2.   This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CAR §1.821(c).

[ ]   3.   A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CAR §1.821(e).

[X]   4.   A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CAR §1.822 and/or §1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing".

[ ]   5.   The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CAR §1.825(d).

[ ]   6.   The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CAR §1.821(e).

[ ]   7.   Other: _____

APPLICANT MUST PROVIDE:

[X]   An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

[X]   An initial or substitute paper copy of the "Sequence Listing", as were as an amendment directing its entry into the specification.

[X]   A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CAR §1.821(e) or §1.821(f) or §1.821(g) or §1.825(b) or §1.825(d).

FOR QUESTIONS REGARDING COMPLIANCE WITH THESE REQUIREMENTS, PLEASE CONTACT:

For Rules Interpretation, call (703) 308-1123
For CRF Submission help, call (703)308-4212
For Patentin Software help, call (703) 557-0400

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE.

~) Deui

1645

See pp. 2,4,6

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            RAW SEQUENCE LISTING          DATE: 09/06/2000
            PATENT APPLICATION:  US/09/446,677   TIME: 11:01:37

            Input Set : A:\Birkell.txt
            Output Set: N:\CRF3\09062000\I446677.raw

            SEQUENCE LISTING
   3 (1) GENERAL INFORMATION:
   5      (i) APPLICANT: BIRKELUND, Svend
   6                     CHRISTIANSEN, Gunna
   7                     HEBSGAARD PEDERSEN, Anna-Sofie
   8                     MYGIND, Per
   9                     KNUDSEN, Katrine
  11     (ii) TITLE OF INVENTION: SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
  12                              PNEUMONIAE
  14    (iii) NUMBER OF SEQUENCES: 30
  16     (iv) CORRESPONDENCE ADDRESS:
  17          (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
  18          (B) STREET: 624 Ninth Street, N.W., Suite 300
  19          (C) CITY: Washington
  20          (D) STATE: D.C.
  21          (E) COUNTRY: USA
  22          (F) ZIP: 20001
  24      (v) COMPUTER READABLE FORM:
  25          (A) MEDIUM TYPE: Floppy disk
  26          (B) COMPUTER: IBM PC compatible
  27          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  28          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  30     (vi) CURRENT APPLICATION DATA:
C--> 31        (A) APPLICATION NUMBER: US/09/446,677
C--> 32        (B) FILING DATE: 24-Mar-2000
C--> 38   (vii) PRIOR APPLICATION DATA:
  35          (A) APPLICATION NUMBER: PCT/DK98/00266
  36          (B) FILING DATE: 19-JUN-1998
  39          (A) APPLICATION NUMBER: DK 0744/97
  40          (B) FILING DATE: 23-JUN-1997
  42   (viii) ATTORNEY/AGENT INFORMATION:
  43          (A) NAME: COOPER, Iver P.
  44          (B) REGISTRATION NUMBER: 28,005
  45          (C) REFERENCE/DOCKET NUMBER: BIRKELUND=1
  47     (ix) TELECOMMUNICATION INFORMATION:
  48          (A) TELEPHONE: 202-628-5197
  49          (B) TELEFAX: 202-737-3528


ERRORED SEQUENCES

 498 (2) INFORMATION FOR SEQ ID NO: 3:
 500      (i) SEQUENCE CHARACTERISTICS:
 501          (A) LENGTH: 2815 base pairs
 502          (B) TYPE: nucleic acid
 503          (C) STRANDEDNESS: single
 504          (D) TOPOLOGY: linear
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,677

DATE: 09/06/2000
TIME: 11:01:37

Input Set : A:\Birkell.txt
Output Set: N:\CRF3\09062000\I446677.raw

Enter "hard return" here to correct.

506   (ii) MOLECULE TYPE: Genomic DNA
508   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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ATGAAATCGC AATTTTCCTG GTTAGTGCTC TCTTCGACAT TGGCATGTTT TACTAGTTGT
      511 ACTAACACAG GCACCTATAC TCCTAAAAAT ACGACTACTG GAATAGACTA TACTCTGACA   180
      512 GGAGATATAA CTCTGCAAAA CCTTGGGGAT TCGGCAGCTT TAACGAAGGG TTGTTTTTCT   240
      513 GACACTACGG AATCTTTAAG CTTTGCCGGT AAGGGGTACT CACTTTCTTT TTTAAATATT   300
      514 AAGTCTAGTG CTGAAGGCGC AGCACTTTCT GTTACAACTG ATAAAAATCT GTCGCTAACA   360
      515 GGATTTTCGA GTCTTACTTT CTTAGCGGCC CCATCATCGG TAATCACAAC CCCCTCAGGA   420
      516 AAAGGTGCAG TTAAATGTGG AGGGGATCTT ACATTTGATA ACAATGGAAC TATTTTATTT   480
      517 AAACAAGATT ACTGTGAGGA AAATGGCGGA GCCATTTCTA CCAAGAATCT TTCTTTGAAA   540
      518 AACAGCACGG GATCGATTTC TTTTGAAGGG AATAAATCGA GCGCAACAGG GAAAAAAGGT   600
      519 GGGGCTATTT GTGCTACTGG TACTGTAGAT ATTACAAATA ATACGGCTCC TACCCTCTTC   660
      520 TCGAACAATA TTGCTGAAGC TGCAGGTGGA GCTATAAATA GCACAGGAAA CTGTACAATT   720
      521 ACAGGGAATA CGTCTCTTGT ATTTTCTGAA AATAGTGTGA CAGCGACCGC AGGAAATGGA   780
      522 GGAGCTCTTT CTGGAGATGC CGATGTTACC ATATCTGGGA ATCAGAGTGT AACTTTCTCA   840
      523 GGAAACCAAG CTGTAGCTAA TGGCGGAGCC ATTTATGCTA AGAAGCTTAC ACTGGCTTCC   900
      524 GGGGGGGGGG GGGGTATCTC CTTTTCTAAC AATATAGTCC AAGGTACCAC TGCAGGTAAT   960
      525 GGTGGAGCCA TTTCTATACT GGCAGCTGGA GAGTGTAGTC TTTCAGCAGA AGCAGGGGAC   1020
      526 ATTACCTTCA ATGGGAATGC CATTGTTGCA ACTACACCAC AAACTACAAA AAGAAATTCT   1080
      527 ATTGACATAG GATCTACTGC AAAGATCACG AATTTACGTG CAATATCTGG GCATAGCATC   1140
      528 TTTTTCTACG ATCCGATTAC TGCTAATACG GCTGCGGATT CTACAGATAC TTTAAATCTC   1200
      529 AATAAGGCTG ATGCAGGTAA TAGTACAGAT TATAGTGGGT CGATTGTTTT TTCTGGTGAA   1260
      530 AAGCTCTCTG AAGATGAAGC AAAAGTTGCA GACAACCTCA CTTCTACGCT GAAGCAGCCT   1320
      531 GTAACTCTAA CTGCAGGAAA TTTAGTACTT AAACGTGGTG TCACTCTCGA TACGAAAGGT   1380
      532 TTTACTCAGA CCGCGGGTTC CTCTGTTATT ATGGATGCGG GCACAACGTT AAAAGCAAGT   1440
      533 ACAGAGGAGG TCACTTTAAC AGGTCTTTCC ATTCCTGTAG ACTCTTTAGG CGAGGGTAAG   1500
      534 AAAGTTGTAA TTGCTGCTTC TGCAGCAAGT AAAAATGTAG CCCTTAGTGG TCCGATTCTT   1560
      535 CTTTTGGATA ACCAAGGGAA TGCTTATGAA AATCACGACT TAGGAAAAAC TCAAGACTTT   1620
      536 TCATTTGTGC AGCTCTCTGC TCTGGGTACT GCAACAACTA CAGATGTTCC AGCGGTTCCT   1680
      537 ACAGTAGCAA CTCCTACGCA CTATGGGTAT CAAGGTACTT GGGGAATGAC TTGGGGTTGAT   1740
      538 GATACCGCAA GCACTCCAAA GACTAAGACA CGCGACATTAG CTTGGACCAA TACAGGCTAC   1800
      539 CTTCCGAATC CTGAGCGTCA AGGACCTTTA GTTCCTAATA GCCTTTGGGG ATCTTTTTCA   1860
      540 GACATCCAAG CGATTCAAGG TGTCATAGAG AGAAGTGCTT TGACTCTTTG TTCAGATCGA   1920
      541 GGCTTCTGGG CTGCGGGAGT CGCCAATTTC TTAGATAAAG ATAAGAAAGG GGAAAAACGC   1980
      542 AAATACCGTC ATAAATCTGG TGGATATGCT ATCGGAGGTG CAGCGCAAAC TTGTTCTGAA   2040
      543 AACTTATTA GCTTTGCCTT TTGCCAACTC TTTGGTAGCG ATAAAGATTT CTTAGTCGCT   2100
      544 AAAAATCATA CTGATACCTA TGCAGGAGCC TTCTATATCC AACACATTAC AGAATGTAGT   2160
      545 GGGTTCATAG GTTGTCTCTT AGATAAACTT CCTGGCTCTT GGAGTCATAA ACCCCTCGTT   2220
      546 TTAGAAGGGC AGCTCGCTTA TAGCCACGTC AGTAATGATC TGAAGACAAA GTATACTGCG   2280
      547 TATCCTGAGG TGAAAGGTTC TTGGGGGAAT AATGCTTTTA ACATGATGTT GGGAGCTTCT   2340
      548 TCTCATTCTT ATCCTGAATA CCTGCATTGT TTTGATACCT ATGCTCCATA CATCAAACTG   2400
      549 AATCTGACCT ATATACGTCA GGACAGCTTC TCGGAGAAAG GTACAGAAGG AAGAGTTCTCT   2460
      550 GATGACAGCA ACCTCTTCAA TTTATCTTTG CCTATAGGGG TGAAGTTTGA GAAGTTCTCT   2520
      551 GATTGTAATG ACTTTTCTTA TGATCTGACT TTATCCTATG TTCCTGATCT TATCCGCAAT   2580
      552 GATCCCAAAT GCACTACAGC ACTTGTAATC AGCGGAGCCT CTTGGGAAAC TTATGCCAAT   2640
      553 AACTTAGCAC GACAGGCCTT GCAAGTGCGT GCAGGCAGTC ACTACGCCTT CTCTCCTATG   2700
      554 TTTGAAGTGC TCGGCCAGTT TGTCTTTGAA GTTCGTGGAT CCTCACGGAT TTATAATGTA   2760
      555 GATCTTGGGG GTAAGTTCCA ATTCTAGGAG CGTCTCTCAT GTCTCAGAAA TTCTG   2815

743 (2) INFORMATION FOR SEQ ID NO: 5:

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745   (i) SEQUENCE CHARACTERISTICS:
746       (A) LENGTH: 3052 base pairs    ─>  See p. 4
747       (B) TYPE: nucleic acid
748       (C) STRANDEDNESS: single
749       (D) TOPOLOGY: linear
751  (ii) MOLECULE TYPE: Genomic DNA
753  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
755 ATGCGATTTT CGCTCTGCGG ATTTCCTCTA GTTTTTTCTT TAACATTGCT CTCAGTCTTC    60
756 GACACTTCTT TGAGTGCTAC TACGATTTCT TTAACCCCAG AAGATAGTTT TCATGGAGAT   120
757 AGTCAGAATG CAGAACGTTC TTATAATGTT CAAGCTGGGG ATGTCTATAG CCTTACTGGT   180
758 GATGTCTCAA TATCTAACGT CGATAACTCT GCATTAAATA AAGCCTGCTT CAATGTGACC   240
759 TCAGGAAGTG TGACGTTCGC AGGAAATCAT CATGGGTTAT ATTTTAATAA TATTTCCTCA   300
760 GGAACTACAA AGGAAGGGGC TGTACTTTGT TGCCAAGATC CTCAAGCAAC GGCACGTTTT   360
761 TCTGGGTTCT CCACGCTCTC TTTTATTCAG AGCCCCGGAG ATATTAAAGA ACAGGGATGT   420
762 CTCTATTCAA AAAATGCACT TATGCTCTTA AACAATTATG TAGTGCGTTT TGAACAAAAC   480
763 CAAAGTAAGA CTAAAGGCGG AGCTATTAGT GGGGCGAATG TTACTATAGT AGGCAACTAC   540
764 GATTCCGTCT CTTTCTATCA GAATGCAGCC ACTTTTGGAG GTGCTATCCA TTCTTCAGGT   600
765 CCCCTACAGA TTGCAGTAAA TCAGGCAGAG ATAAGATTTG CACAAAATAC TGCCAAGAAT   660
766 GGTTCTGGAG GGGCTTTGTA CTCCGATGGT GATATTGATA TTGATCAGAA TGCTTATGTT   720
767 CTATTTCGAG AAAATGAGGC ATTGACTACT GCTATAGGTA AGGGAGGGGC TGTCTGTTGT   780
768 CTTCCCACTT CAGGAAGTAG TACTCCAGTT CCTATTGTGA CTTTCTCTGA CAATAAACAG   840
769 TTAGTCTTTG AAAGAAACCA TTCCATAATG GGTGGCGGAG CCATTTATGC TAGGAAACTT   900
770 AGCATCTCTT CAGGAGGTCC TACTCTATTT ATCAATAATA TATCATATGC AAATTCGCAA   960
771 AATTTAGGTG GAGCTATTGC CATTGATACT GGAGGGGGAGA TCAGTTTATC AGCAGAGAAA  1020
772 GGAACAATTA CATTCCAAGG AAACCGGACG AGCTTACCGT TTTTGAATGG CATCCATCTT  1080
773 TTACAAAATG CTAAATTCCT GAAATTACAG GCGAGAAATG GATGCTCTAT AGAATTTTAT  1140
774 GATCCTATTA CTTCTGAAGC AGATGGGTCT ACCCAATTGA ATATCAACGA AGATCCTAAA  1200
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788 GAGATCACAC CTAAGCACTA TACTTCGATG GCATTTTCCC AACTCTTTAG TAGAGACAAG  2040
789 GACTATGCGG TTTCCAACAA CGAATACAGA ATGTATTTAG GATCGTATCT CTATCAATAT  2100
790 ACAACCTCCC TAGGGAATAT TTTCCGTTAT GCTTCGCGTA ACCCTAATGT AAACGTCGGG  2160
791 ATTCTCTCAA GAAGGTTTCT. TCAAAATCCT CTTATGATTT TTCATTTTTT GTGTGCTTAT  2220
792 GGTCATGCCA CCAATGATAT GAAAACAGAC TACGCAAATT TCCCTATGGT GAAAAACAGC  2280
793 TGGAGAAACA ATTGTTGGGC TATAGAGTGC GGAGGGAGCA TGCCTCTATT GGTATTTGAG  2340
794 AACGGAAGAC TTTTCCAAGG TGCCATCCCA TTTATGAAAC TACAATTAGT TTATGCTTAT  2400
795 CAGGGAGATT TCAAAGAGAC GACTGCAGAT GGCCGTAGAT TTAGTAATGG GAGTTTAACA  2460
796 TCGATTTCTG TACCTCTAGG CATACGCTTT GAGAAGCTGG CACTTTCTCA GGATGTACTC  2520
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,677

DATE: 09/06/2000
TIME: 11:01:37

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Output Set: N:\CRF3\09062000\I446677.raw

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800 GGAAGTATAG AATGCCGCCC CCATGCTAGG AATTATAATA TAAACTGTGG AAGCAAATTT   2760
801 CGTTTTTAGA AGGTTTCCAT TGCCTGTGTG GTTCCGGATC TTAACTATAA ATCCTGGACT   2820
802 ATGGATCATA GGCATTGGGT TTCTCGAACT TGTGTGGAGA ATAACGACAT TTTATATGCA   2880
803 TAACGGAATA CTCGTATCAC CTCAGCCCCT AGAGACATTC TTTAGGGGTT CTTTATTTGT   2940
804 CTAAACTTCG TATTTTATCG AGAATCCTTT ACGTTCTTGG TTTGCTTGTC TCCGAGGAGT   3000
E--> 805 TCTCTAACGA ATCATAGGGA TTCCAGGGTT CTGTTCCTTG AGTCCTTTGG A   (3052)
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(handwritten margin note:) Number of bases conflict, 3052 listed, 3051 fou...

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2597 (2) INFORMATION FOR SEQ ID NO: 24:
2599      (i) SEQUENCE CHARACTERISTICS:
2600          (A) LENGTH: 946 amino acids
2601          (B) TYPE: amino acid
2602          (C) STRANDEDNESS: single
2603          (D) TOPOLOGY: linear
2605      (ii) MOLECULE TYPE: peptide
2607      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
2609 Met Lys Thr Ser Val Ser Met Leu Leu Ala Leu Leu Cys Ser Gly Ala
2610   1               5                   10                  15
2612 Ser Ser Ile Val Leu His Ala Ala Thr Thr Pro Leu Asn Pro Glu Asp
2613              20                  25                  30
2615 Gly Phe Ile Gly Glu Gly Asn Thr Asn Thr Phe Ser Pro Lys Ser Thr
2616          35                  40                  45
2618 Thr Asp Ala Ala Gly Thr Thr Tyr Ser Leu Thr Gly Glu Val Leu Phe
2619      50                  55                  60
2621 Ile Asp Pro Gly Lys Gly Gly Ser Ile Thr Gly Thr Cys Phe Val Glu
2622  65                  70                  75                  80
2624 Thr Ala Gly Asp Leu Thr Phe Leu Gly Asn Gly Asn Thr Leu Lys Phe
2625              85                  90                  95
2627 Leu Ser Val Asp Ala Gly Ala Asn Ile Ala Val Ala His Val Gln Gly
2628             100                 105                 110
2630 Ser Lys Asn Leu Ser Phe Thr Asp Phe Leu Ser Leu Val Ile Thr Glu
2631         115                 120                 125
2633 Ser Pro Lys Ser Ala Val Ser Thr Gly Lys Gly Ser Leu Val Ser Ser
2634     130                 135                 140
2636 Gly Ala Val Gln Leu Gln Asp Ile Asn Thr Leu Val Leu Thr Ser Asn
2637 145                 150                 155                 160
2639 Ala Ser Val Glu Asp Gly Gly Val Ile Lys Gly Asn Ser Cys Leu Ile
2640             165                 170                 175
2642 Gln Gly Ile Lys Asn Ser Ala Ile Phe Gly Gln Asn Thr Ser Ser Lys
2643         180                 185                 190
2645 Lys Gly Gly Ala Ile Ser Thr Thr Gln Gly Leu Thr Ile Glu Asn Asn
2646     195                 200                 205
2648 Leu Gly Thr Leu Lys Phe Asn Glu Asn Lys Ala Val Thr Ser Gly Gly
2649 210                 215                 220
2651 Ala Leu Asp Leu Gly Ala Ala Ser Thr Phe Thr Ala Asn His Glu Leu
2652 225                 230                 235                 240
2654 Ile Phe Ser Gln Asn Lys Thr Ser Gly Asn Ala Ala Asn Gly Gly Ala
2655             245                 250                 255
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2657 Ile Asn Cys Ser Gly Asp Leu Thr Phe Thr Asp Asn Thr Ser Leu Leu
2658              260                    265                    270
2660 Leu Gln Glu Asn Ser Thr Met Gln Asp Gly Gly Ala Leu Cys Ser Thr
2661     275                    280                    285
2663 Gly Thr Ile Ser Ile Thr Gly Ser Asp Ser Ile Asn Val Ile Gly Asn
2664     290                    295                    300
2666 Thr Ser Gly Gln Lys Gly Gly Ala Ile Ser Ala Ala Ser Leu Lys Ile
2667 305                    310                    315                    320
2669 Leu Gly Gly Gln Gly Gly Ala Leu Phe Ser Asn Asn Val Val Thr His
2670                    325                    330                    335
2672 Ala Thr Pro Leu Gly Gly Ala Ile Phe Ile Asn Thr Gly Gly Ser Leu
2673              340                    345                    350
2675 Gln Leu Phe Thr Gln Gly Gly Asp Ile Val Phe Glu Gly Asn Gln Val
2676              355                    360                    365
2678 Thr Thr Thr Ala Pro Asn Ala Thr Thr Lys Arg Asn Val Ile His Leu
2679     370                    375                    380
2681 Glu Ser Thr Ala Lys Trp Thr Gly Leu Ala Ala Ser Gln Gly Asn Ala
2682 385                    390                    395                    400
2684 Ile Tyr Phe Tyr Asp Pro Ile Thr Thr Asn Asp Thr Gly Ala Ser Asp
2685              405                    410                    415
2687 Asn Leu Arg Ile Asn Glu Val Ser Ala Asn Gln Lys Leu Ser Gly Ser
2688              420                    425                    430
2690 Ile Val Phe Ser Gly Glu Arg Leu Ser Thr Ala Glu Ala Ile Ala Glu
2691     435                    440                    445
2693 Asn Leu Thr Ser Arg Ile Asn Gln Pro Val Thr Leu Val Glu Gly Ser
2694     450                    455                    460
2696 Leu Glu Leu Lys Gln Gly Val Thr Leu Ile Thr Gln Gly Phe Ser Gln
2697 465                    470                    475                    480
2699 Glu Pro Glu Ser Thr Leu Leu Leu Asp Leu Gly Thr Ser Leu Gln Ala
2700              485                    490                    495
2702 Ser Thr Glu Asp Ile Val Ile Thr Asn Ser Ser Ile Asn Ala Asp Thr
2703              500                    505                    510
2705 Ile Tyr Gly Lys Asn Pro Ile Asn Ile Val Ala Ser Ala Ala Asn Lys
2706     515                    520                    525
2708 Asn Ile Thr Leu Thr Gly Thr Leu Ala Leu Val Asn Ala Asp Gly Ala
2709     530                    535                    540
2711 Leu Tyr Glu Asn His Thr Leu Gln Asp Ser Gln Asp Tyr Ser Phe Val
2712 545                    550                    555                    560
2714 Lys Leu Ser Pro Gly Ala Gly Gly Thr Ile Ile Thr Gln Asp Ala Ser
2715              565                    570                    575
2717 Gln Lys Leu Leu Glu Val Ala Pro Ser Arg Pro His Tyr Gly Tyr Gln
2718              580                    585                    590
2720 Gly His Trp Asn Val Gln Val Ile Pro Gly Thr Gly Thr Gln Pro Ser
2721     595                    600                    605
2723 Gln Ala Asn Leu Glu Trp Val Arg Thr Gly Tyr Leu Pro Asn Pro Glu
2724 610                    615                    620
2726 Arg Gln Gly Phe Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Val Asp
2727 625                    630                    635                    640
2729 Gln Arg Ala Ile Gln Glu Ile Met Val Asn Ser Ser Gln Ile Leu Cys
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                             645                    650                    655
2730                                           Ile Ala Asn Phe Leu His Arg
2732 Gln Glu Arg Gly Val Trp Gly Ala Gly            665             670
2733                     660         His Ser Gly Val Gly Tyr Leu
2735 Asp Lys Ile Asn Glu His Gly Tyr Arg            680             685
2736                 675         Asp Ala Thr Ile Asn Ala Ala
2738 Val Gly Val Gly Thr His Ala Phe Ser            700
2739     690             695         Tyr Val Val Ser Lys Asn
2741 Phe Cys Gln Leu Phe Ser Arg Asp Lys Asp        715             720
2742 705             710         Phe Leu Glu Asp Thr Leu Glu
2744 His Gly Thr Ser Tyr Ser Gly Val Val            730             735
2745                 725         Thr Asp Ser Ser Ser Glu Ala Cys
2747 Phe Arg Ser Pro Gln Gly Phe Tyr Thr            745             750
2748             740         Gln Leu Ser Tyr Ser His Arg
2750 Cys Asn Gln Val Val Thr Ile Asp Met            760             765
2751         755         Thr Thr Tyr Pro Glu Ala Gln Gly
2753 Asn Asn Asp Met Lys Thr Lys Tyr                780
2754     770             775         Phe Gly Ala Thr Thr Tyr
2756 Ser Trp Ala Asn Asp Val Phe Gly Leu Glu        795             800
2757 785             790         Tyr Tyr Ser Pro Phe Leu
2759 Tyr Tyr Pro Asn Ser Thr Phe Leu Phe Asp        810             815
2760             805         Glu Asp Phe Lys Glu Thr Gly
2762 Arg Leu Gln Cys Thr Tyr Ala His Gln            825             830
2763         820         Gly Asp Leu Phe Asn Leu Ala Val
2765 Gly Glu Val Arg His Phe Thr Ser                840             845
2766     835         Arg Phe Ser Asp Cys Lys Arg Gly Ser
2768 Pro Ile Gly Val Lys Phe Glu                    855             860
2769 850             Tyr Val Pro Asp Val Ile Arg Lys Asp Pro
2771 Tyr Glu Leu Thr Leu Ala                        870             875             880
2772 865             Thr Trp Ser Thr His Gly
2774 Lys Ser Thr Ala Thr Leu Ala Ser Gly Ala        890             895
2775             885         Arg Leu Gly Asn His Cys
2777 Asn Asn Leu Ser Arg Gln Gly Leu Gln Leu        905             910
2778             900         Ser His Gly Ala Ile Glu Leu
2780 Leu Ile Asn Pro Gly Ile Glu Val Phe            920             925
2781         915         Leu Gly Gly Lys Tyr Arg
2783 Arg Gly Ser Ser Arg Asn Tyr Asn Ile Asn        940
2784         930             935
2786 Phe
E--> 2787 945
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945 amino acids found, 946 listed as length.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/446,677

DATE: 09/06/2000
TIME: 11:01:39

Input Set : A:\Birkell.txt
Output Set: N:\CRF3\09062000\I446677.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:38 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:510 M:320 E: (1) Wrong Nucleic Acid Designator, 2
L:805 M:254 E: No. of Bases conflict, Input:3052 Counted:3051 SEQ:5
L:805 M:204 E: No. of Bases differ, LENGTH:Input:3052 Counted:3051 SEQ:5
L:2454 M:220 C: Keyword misspelled or invalid format, [(ii) MOLECULE TYPE:]
L:2787 M:203 E: No. of Seq. differs, LENGTH:Input:946 Found:945 SEQ:24